



SEQUENCE LISTING

<110> Kato, Seishi  
Sekine, Shingo

<120> HUMAN PROTEINS HAVING TRANSMEMBRANE DOMAINS AND  
CDNAS ENCODING THESE PROTEINS

<130> 1997.17300.2

<140> 10/616,942

<141> 2003-07-11

<150> 09/529,100

<151> 2000-08-21

<150> JP 0276269

<151> 1997-10-08

<150> PCT/JP98/04474

<151> 1998-10-05

<160> 30

<170> PatentIn Ver. 2.0

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Leu Tyr Leu Gly Asp Gly Tyr Val Ile Asn Ile Ala Pro Val Asp Gly  
35 40 45

Ile Pro Ala Ser Phe Thr Ser Ala Lys Ser Val Phe Ser Ser Lys Ala  
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Leu Val Lys Met Gln Leu Leu Lys Asp Val Val Gly Asn Asp Thr Tyr  
65 70 75 80

Arg Ile Asn Asn Lys Tyr Asp Glu Thr Tyr Pro Pro Leu Pro Val Glu  
85 90 95

Glu Ile Ile Lys Arg Ser Glu Phe Val Ile Gly Gln Glu Val Ala Tyr  
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Asn Leu Leu Val Asn Asn Cys Glu His Phe Val Thr Leu Leu Arg Tyr  
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Gly Glu Gly Val Ser Glu Gln Ala Asn Arg Ala Ile Ser Thr Val Glu  
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Gln Val Glu Lys Ala Lys Val Glu Val Gly Val Ala Thr Ala Leu Gly  
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 Val Thr Leu Thr Ala Ala Asn Val Thr Val Ser Leu Pro Val Arg Gly  
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 Cys Val Gln Asp Glu Phe Cys Thr Arg Asp Gly Val Thr Gly Pro Gly  
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 Asp Arg Ser Asn Ser Gly Gln Tyr Pro Ala Lys Gly Gly Pro Gln Gln  
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ctgggagcac gcacgcacaa ctacgggatt ggcgccgccg cctgcgtgta ctttggcata 360  
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ttc cgt cct ggc tat cag cac tgg gcc ctg tac ttg ggt gat ggt tac 328

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Val	Ile	Asn	Ile	Ala	Pro	Val	Asp	Gly	Ile	Pro	Ala	Ser	Phe	Thr	Ser	55	
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Ala	Lys	Ser	Val	Phe	Ser	Ser	Lys	Ala	Leu	Val	Lys	Met	Gln	Leu	Leu	70	
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aag	gat	gtt	gtg	gga	aat	gac	aca	tac	aga	ata	aac	aat	aaa	tac	gat	472	
Lys	Asp	Val	Val	Gly	Asn	Asp	Thr	Tyr	Arg	Ile	Asn	Asn	Lys	Tyr	Asp	85	
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Phe	Val	Ile	Gly	Gln	Glu	Val	Ala	Tyr	Asn	Leu	Leu	Val	Asn	Asn	Cys	115	
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Tyr																	
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Leu	Tyr	Leu	Gly	Asp	Gly	Tyr	Val	Ile	Asn	Ile	Ala	Pro	Val	Asp	Gly		
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Ile	Pro	Ala	Ser	Phe	Thr	Ser	Ala	Lys	Ser	Val	Phe	Ser	Ser	Lys	Ala		
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Glu Ile Ile Lys Arg Ser Glu Phe Val Ile Gly Gln Glu Val Ala Tyr  
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Asn Leu Leu Val Asn Asn Cys Glu His Phe Val Thr Leu Leu Arg Tyr  
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Gly Glu Gly Val Ser Glu Gln Ala Asn Arg Ala Ile Ser Thr Val Glu  
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Pro Gly Asp Leu Ile Glu Ile Phe Arg Leu Gly Tyr Glu His Trp Ala  
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ctg tat ata gga gat ggc tac gtg atc cat ctg gct cct cca agt gag 147  
Leu Tyr Ile Gly Asp Gly Tyr Val Ile His Leu Ala Pro Pro Ser Glu  
30 35 40  
tac ccc ggg gct ggc tcc tcc agt gtc ttc tca gtc ctg agc aac agt 195  
Tyr Pro Gly Ala Gly Ser Ser Ser Val Phe Ser Val Leu Ser Asn Ser  
45 50 55  
gca gag gtg aaa cgg gag cgc ctg gaa gat gtg gtg gga ggc tgt tgc 243  
Ala Glu Val Lys Arg Glu Arg Leu Glu Asp Val Val Gly Gly Cys Cys  
60 65 70  
tat cgg gtc aac aac agc ttg gac cat gag tac caa cca cgg ccc gtg 291  
Tyr Arg Val Asn Asn Ser Leu Asp His Glu Tyr Gln Pro Arg Pro Val  
75 80 85  
gag gtg atc atc agt tct gcg aag gag atg gtt ggt cag aag atg aag 339  
Glu Val Ile Ile Ser Ser Ala Lys Glu Met Val Gly Gln Lys Met Lys  
90 95 100 105  
tac agt att gtg agc agg aac tgt gag cac ttt gtc acc cag ctg aga 387  
Tyr Ser Ile Val Ser Arg Asn Cys Glu His Phe Val Thr Gln Leu Arg  
110 115 120  
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Tyr Gly Lys Ser Arg Cys Lys Gln Val Glu Lys Ala Lys Val Glu Val  
125 130 135

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 Ala Ile Arg Arg Tyr Gln Lys Lys Ala Thr Ala  
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 Leu Glu Asp Val Val Gly Gly Cys Cys Tyr Arg Val Asn Asn Ser Leu  
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 Lys Glu Met Val Gly Gln Lys Met Lys Tyr Ser Ile Val Ser Arg Asn  
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 Cys Glu His Phe Val Thr Gln Leu Arg Tyr Gly Lys Ser Arg Cys Lys  
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ccc gat ggc acc gat tgc cac cgc aaa gcc tac agc acc acc agt att 157  
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gcc agc gtc gct ggc ctg acc gcc gct gcc tac aga gtc aca ctc aat 205  
Ala Ser Val Ala Gly Leu Thr Ala Ala Tyr Arg Val Thr Leu Asn  
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cct ccg ggc acc ttc ctt gaa gga gtg gct aag gtt gga caa tac acg 253  
Pro Pro Gly Thr Phe Leu Glu Gly Val Ala Lys Val Gly Gln Tyr Thr  
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Ser Ala His Val Arg Glu Lys Pro Asp Asp Pro Leu Asn Tyr Phe Leu  
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Val Lys Met Gly Arg Leu Glu Gly Trp Glu Val Phe Ala Lys Pro Lys  
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Phe Leu Glu Gly Val Ala Lys Val Gly Gln Tyr Thr Phe Thr Ala Ala  
Page 11

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Arg Glu Lys Pro Asp Asp Pro Leu Asn Tyr Phe Leu Gly Gly Cys Ala				
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Gly Gly Leu Thr Leu Gly Ala Arg Thr His Asn Tyr Gly Ile Gly Ala				
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Pro Asp Glu Leu Leu Pro Lys Gly Asp Ala Glu Lys Pro Glu Glu Glu	
20 25 30	
ctg gag gag gac gac gat gag gag cta gat gag acc ctg tcg gag aga	145
Leu Glu Glu Asp Asp Asp Glu Glu Leu Asp Glu Thr Leu Ser Glu Arg	
35 40 45	
cta tgg ggc ctg acg gag atg ttt ccg gag agg gtc cgg tcc gcg gcc	193
Leu Trp Gly Leu Thr Glu Met Phe Pro Glu Arg Val Arg Ser Ala Ala	
50 55 60	
gga gcc act ttt gat ctt tcc ctc ttt gtg gct cag aaa atg tac agg	241
Gly Ala Thr Phe Asp Leu Ser Leu Phe Val Ala Gln Lys Met Tyr Arg	
65 70 75	
ttt tcc agg gca gcc ttg tgg att ggg acc act tcc ttt atg atc ctg	289
Phe Ser Arg Ala Ala Leu Trp Ile Gly Thr Thr Ser Phe Met Ile Leu	
80 85 90 95	
gtt ctt ccc gtt gtc ttt gag acg gag aag ttg caa atg gag caa cag	337
Val Leu Pro Val Val Phe Glu Thr Glu Lys Leu Gln Met Glu Gln Gln	
100 105 110	
cag caa ctg cag cag cgg cag ata ctt cta gga cct aac aca ggg ctc	385
Gln Gln Leu Gln Gln Arg Gln Ile Leu Leu Gly Pro Asn Thr Gly Leu	
115 120 125	
tca gga gga atg cca ggg gct cta ccc tca ctt cct gga aag atc	430
Ser Gly Gly Met Pro Gly Ala Leu Pro Ser Leu Pro Gly Lys Ile	
130 135 140	

tagattgtta ttgctgtttg agctgtctca gtgggataag tttgaaattc aagtgtttga 490  
 actgctgata atttggattt tttttttttt ttttaacttt ggcacattga tctatctaaa 550  
 cccggtgggg agaattatcc ccacattgtc tcatggaaag actcaacttg caactgtgcc 610  
 ctccacacta tccttacttc tgtctccact ctgataccag agtgcagcca tgcagacggt 670  
 tattccagct ctggtcaccc gactcctttc accaaattgc tcctaactgg aagatctcac 730  
 tttccccttg tggggtagga accgatgcc a gtgggagggg tgtgcccctg accattaacg 790  
 actgtttttt tttttttttt ttaaagaatg gagttgttgg ggcgggacat gcacacaatg 850  
 tgaaacagac aaaatgcatt acacctgtag tgtaaagtgg ccactatgaa tccctatgta 910  
 tgagaggagg gaggcaggct gcagcttcag ccacagaatg gggactatgg aagacagcag 970  
 gagctcattt cctctgcaca tttcggctgt tagacctgtg tgtgtgttta aaaaaagaga 1030  
 agtcagtgtc cactttttgt atttaaatat taaaaatgat tccaactg 1078

<210> 20  
 <211> 142  
 <212> PRT  
 <213> Homo sapiens

<400> 20  
 Met Ala Ala Ala Val Ala Ala Ala Gly Ala Gly Glu Pro Gln Ser Pro  
 1 5 10 15  
 Asp Glu Leu Leu Pro Lys Gly Asp Ala Glu Lys Pro Glu Glu Glu Leu  
 20 25 30  
 Glu Glu Asp Asp Asp Glu Glu Leu Asp Glu Thr Leu Ser Glu Arg Leu  
 35 40 45  
 Trp Gly Leu Thr Glu Met Phe Pro Glu Arg Val Arg Ser Ala Ala Gly  
 50 55 60  
 Ala Thr Phe Asp Leu Ser Leu Phe Val Ala Gln Lys Met Tyr Arg Phe  
 65 70 75 80  
 Ser Arg Ala Ala Leu Trp Ile Gly Thr Thr Ser Phe Met Ile Leu Val  
 85 90 95  
 Leu Pro Val Val Phe Glu Thr Glu Lys Leu Gln Met Glu Gln Gln Gln  
 100 105 110  
 Gln Leu Gln Gln Arg Gln Ile Leu Leu Gly Pro Asn Thr Gly Leu Ser  
 115 120 125  
 Gly Gly Met Pro Gly Ala Leu Pro Ser Leu Pro Gly Lys Ile  
 130 135 140

<210> 21  
 <211> 1310  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS

<222> (82)..(1119)

<400> 21

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actcatcctg ggctcaggta agagggcccg agctcggagg cggcacatcc aggggggacg 60
ccaagggagc aggacggagc c atg gac ccc gcc agg aaa gca ggt gcc cag 111
                        Met Asp Pro Ala Arg Lys Ala Gly Ala Gln
                        1          5          10
gcc atg atc tgg act gca ggc tgg ctg ctg ctg ctg ctt cgc gga 159
Ala Met Ile Trp Thr Ala Gly Trp Leu Leu Leu Leu Leu Arg Gly
                        15          20          25
gga gcg cag gcc ctg gag tgc tac agc tgc gtg cag aaa gca gat gac 207
Gly Ala Gln Ala Leu Glu Cys Tyr Ser Cys Val Gln Lys Ala Asp Asp
                        30          35          40
gga tgc tcc ccg aac aag atg aag aca gtg aag tgc gcg ccg ggc gtg 255
Gly Cys Ser Pro Asn Lys Met Lys Thr Val Lys Cys Ala Pro Gly Val
                        45          50          55
gac gtc tgc acc gag gcc gtg ggg gcg gtg gag acc atc cac gga caa 303
Asp Val Cys Thr Glu Ala Val Gly Ala Val Glu Thr Ile His Gly Gln
                        60          65          70
ttc tcg ctg gca gtg cgg ggt tgc ggt tcg gga ctc ccc ggc aag aat 351
Phe Ser Leu Ala Val Arg Gly Cys Gly Ser Gly Leu Pro Gly Lys Asn
                        75          80          85
gac cgc ggc ctg gat ctt cac ggg ctt ctg gcg ttc atc cag ctg cag 399
Asp Arg Gly Leu Asp Leu His Gly Leu Leu Ala Phe Ile Gln Leu Gln
                        95          100          105
caa tgc gct cag gat cgc tgc aac gcc aag ctc aac ctc acc tcg cgg 447
Gln Cys Ala Gln Asp Arg Cys Asn Ala Lys Leu Asn Leu Thr Ser Arg
                        110          115          120
gcg ctc gac ccg gca ggt aat gag agt gca tac ccg ccc aac ggc gtg 495
Ala Leu Asp Pro Ala Gly Asn Glu Ser Ala Tyr Pro Pro Asn Gly Val
                        125          130          135
gag tgc tac agc tgt gtg ggc ctg agc cgg gag gcg tgc cag ggt aca 543
Glu Cys Tyr Ser Cys Val Gly Leu Ser Arg Glu Ala Cys Gln Gly Thr
                        140          145          150
tcg ccg ccg gtc gtg agc tgc tac aac gcc agc gat cat gtc tac aag 591
Ser Pro Pro Val Val Ser Cys Tyr Asn Ala Ser Asp His Val Tyr Lys
                        155          160          165
ggc tgc ttc gac ggc aac gtc acc ttg acg gca gct aat gtg act gtg 639
Gly Cys Phe Asp Gly Asn Val Thr Leu Thr Ala Ala Asn Val Thr Val
                        175          180          185
tcc ttg cct gtc cgg ggc tgt gtc cag gat gaa ttc tgc act cgg gat 687
Ser Leu Pro Val Arg Gly Cys Val Gln Asp Glu Phe Cys Thr Arg Asp
                        190          195          200
gga gta aca ggc cca ggg ttc acg ctc agt ggc tcc tgt tgc cag ggg 735
Gly Val Thr Gly Pro Gly Phe Thr Leu Ser Gly Ser Cys Cys Gln Gly
                        205          210          215
tcc cgc tgt aac tct gac ctc cgc aac aag acc tac ttc tcc cct cga 783
Ser Arg Cys Asn Ser Asp Leu Arg Asn Lys Thr Tyr Phe Ser Pro Arg
                        220          225          230
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atc cca ccc ctt gtc cgg ctg ccc cct cca gag ccc acg act gtg gcc	831
Ile Pro Pro Leu Val Arg Leu Pro Pro Pro Glu Pro Thr Thr Val Ala	
235 240 245 250	
tca acc aca tct gtc acc act tct acc tcg gcc cca gtg aga ccc aca	879
Ser Thr Thr Ser Val Thr Thr Ser Thr Ser Ala Pro Val Arg Pro Thr	
255 260 265	
tcc acc acc aaa ccc atg cca gcg cca acc agt cag act ccg aga cag	927
Ser Thr Thr Lys Pro Met Pro Ala Pro Thr Ser Gln Thr Pro Arg Gln	
270 275 280	
gga gta gaa cac gag gcc tcc cgg gat gag gag ccc agg ttg act gga	975
Gly Val Glu His Glu Ala Ser Arg Asp Glu Glu Pro Arg Leu Thr Gly	
285 290 295	
ggc gcc gct ggc cac cag gac cgc agc aat tca ggg cag tat cct gca	1023
Gly Ala Ala Gly His Gln Asp Arg Ser Asn Ser Gly Gln Tyr Pro Ala	
300 305 310	
aaa ggg ggg ccc cag cag ccc cat aat aaa ggc tgt gtg gct ccc aca	1071
Lys Gly Gly Pro Gln Gln Pro His Asn Lys Gly Cys Val Ala Pro Thr	
315 320 325 330	
gct gga ttg gca gcc ctt ctg ttg gcc gtg gct gct ggt gtc cta ctg	1119
Ala Gly Leu Ala Ala Leu Leu Ala Val Ala Ala Gly Val Leu Leu	
335 340 345	
tgagcttctc cacctggaaa tttccctctc acctacttct ctggccctgg gtaccctctc	1179
tctcatcact tcctgttccc accactggac tgggctggcc cagcccctgt ttttccaaca	1239
ttccccagta tccccagctt ctgctgcgct ggtttgcggc tttgggaaat aaaataccgt	1299
tgtatatatt c	1310

<210> 22  
 <211> 346  
 <212> PRT  
 <213> Homo sapiens

<400> 22  
 Met Asp Pro Ala Arg Lys Ala Gly Ala Gln Ala Met Ile Trp Thr Ala  
 1 5 10 15  
 Gly Trp Leu Leu Leu Leu Leu Leu Arg Gly Gly Ala Gln Ala Leu Glu  
 20 25 30  
 Cys Tyr Ser Cys Val Gln Lys Ala Asp Asp Gly Cys Ser Pro Asn Lys  
 35 40 45  
 Met Lys Thr Val Lys Cys Ala Pro Gly Val Asp Val Cys Thr Glu Ala  
 50 55 60  
 Val Gly Ala Val Glu Thr Ile His Gly Gln Phe Ser Leu Ala Val Arg  
 65 70 75 80  
 Gly Cys Gly Ser Gly Leu Pro Gly Lys Asn Asp Arg Gly Leu Asp Leu  
 85 90 95  
 His Gly Leu Leu Ala Phe Ile Gln Leu Gln Gln Cys Ala Gln Asp Arg  
 100 105 110

Cys Asn Ala Lys Leu Asn Leu Thr Ser Arg Ala Leu Asp Pro Ala Gly  
 115 120 125  
 Asn Glu Ser Ala Tyr Pro Pro Asn Gly Val Glu Cys Tyr Ser Cys Val  
 130 135 140  
 Gly Leu Ser Arg Glu Ala Cys Gln Gly Thr Ser Pro Pro Val Val Ser  
 145 150 155 160  
 Cys Tyr Asn Ala Ser Asp His Val Tyr Lys Gly Cys Phe Asp Gly Asn  
 165 170 175  
 Val Thr Leu Thr Ala Ala Asn Val Thr Val Ser Leu Pro Val Arg Gly  
 180 185 190  
 Cys Val Gln Asp Glu Phe Cys Thr Arg Asp Gly Val Thr Gly Pro Gly  
 195 200 205  
 Phe Thr Leu Ser Gly Ser Cys Cys Gln Gly Ser Arg Cys Asn Ser Asp  
 210 215 220  
 Leu Arg Asn Lys Thr Tyr Phe Ser Pro Arg Ile Pro Pro Leu Val Arg  
 225 230 235 240  
 Leu Pro Pro Pro Glu Pro Thr Thr Val Ala Ser Thr Thr Ser Val Thr  
 245 250 255  
 Thr Ser Thr Ser Ala Pro Val Arg Pro Thr Ser Thr Thr Lys Pro Met  
 260 265 270  
 Pro Ala Pro Thr Ser Gln Thr Pro Arg Gln Gly Val Glu His Glu Ala  
 275 280 285  
 Ser Arg Asp Glu Glu Pro Arg Leu Thr Gly Gly Ala Ala Gly His Gln  
 290 295 300  
 Asp Arg Ser Asn Ser Gly Gln Tyr Pro Ala Lys Gly Gly Pro Gln Gln  
 305 310 315 320  
 Pro His Asn Lys Gly Cys Val Ala Pro Thr Ala Gly Leu Ala Ala Leu  
 325 330 335  
 Leu Leu Ala Val Ala Ala Gly Val Leu Leu  
 340 345

<210> 23  
 <211> 781  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (342)..(539)

<400> 23  
 caattcccgt tggtgcgttg cgtttccttc ctctttcact ccgcgctcac ggcggcggcc 60  
 aaagcggcgg cgacggcggc gcgagaacga cccggcggcc agttctcttc ctctgcgca 120  
 cctgccctgc tcggtcagtc agtcggcggc cggcgcccgg cttgtgctca gacctcgcgc 180  
 ttgcggcggc caggcccagc ggccgtagct agcgtctggc ctgagaacct cggcgctccg 240



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gcggcgcggg caccacgagc ggagcctcgc agcggctcca gaggaggcag gcgagtgagc 300
gagtccgagg ggtggccggg gcaggtggtg gcgccgcgaa g atg gtc gcc aag caa 356
                                     Met Val Ala Lys Gln
                                     1 5
agg atc cgt atg gcc aac gag aag cac agc aag aac atc acc cag cgc 404
Arg Ile Arg Met Ala Asn Glu Lys His Ser Lys Asn Ile Thr Gln Arg
                                     10 15 20
ggc aac gtc gcc aag acc tcg aga aat gcc ccc gaa gag aag gcg tct 452
Gly Asn Val Ala Lys Thr Ser Arg Asn Ala Pro Glu Glu Lys Ala Ser
                                     25 30 35
gta gga ccc tgg tta ttg gct ctc ttc att ttt gtt gtc tgt ggt tct 500
Val Gly Pro Trp Leu Leu Ala Leu Phe Ile Phe Val Val Cys Gly Ser
                                     40 45 50
gca att ttc cag att att caa agt atc agg atg ggc atg tgaagtgact 549
Ala Ile Phe Gln Ile Ile Gln Ser Ile Arg Met Gly Met
                                     55 60 65
gaccttaaga tgtttccatt ctctgtgaa ttttaacttg aactcattcc tgatgtttga 609
taccctgggtt gaaaacaatt cagtaaagca tcctgcctca gaatgacttt cctatcatgc 669
ttcatgtgtc attccaaggt ttcttcatga gtcattccaa gttttctagt ccataccaca 729
gtgccttgca aaaaacacca catgaataaa gcaataaaat ttgattgtta ag 781

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<210> 24
<211> 66
<212> PRT
<213> Homo sapiens

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<400> 24
Met Val Ala Lys Gln Arg Ile Arg Met Ala Asn Glu Lys His Ser Lys
 1 5 10 15
Asn Ile Thr Gln Arg Gly Asn Val Ala Lys Thr Ser Arg Asn Ala Pro
 20 25 30
Glu Glu Lys Ala Ser Val Gly Pro Trp Leu Leu Ala Leu Phe Ile Phe
 35 40 45
Val Val Cys Gly Ser Ala Ile Phe Gln Ile Ile Gln Ser Ile Arg Met
 50 55 60
Gly Met
 65

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<210> 25
<211> 14
<212> DNA
<213> Artificial Sequence

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<220>
<223> Description of Artificial Sequence: chimeric
      DNA-RNA oligonucleotide

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<400> 25

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ggggaattcg agga

14

<210> 26  
<211> 162  
<212> PRT  
<213> Homo sapiens

<400> 26

Met Arg Ala Pro Ile Pro Glu Pro Lys Pro Gly Asp Leu Ile Glu Ile  
1 5 10 15  
Phe Arg Pro Phe Tyr Arg His Trp Ala Ile Tyr Val Gly Asp Gly Tyr  
20 25 30  
Val Val His Leu Ala Pro Pro Ser Glu Val Ala Gly Ala Gly Ala Ala  
35 40 45  
Ser Val Met Ser Ala Leu Thr Asp Lys Ala Ile Val Lys Lys Glu Leu  
50 55 60  
Leu Tyr Asp Val Ala Gly Ser Asp Lys Tyr Gln Val Asn Asn Lys His  
65 70 75 80  
Asp Asp Lys Tyr Ser Pro Leu Pro Cys Thr Lys Ile Ile Gln Arg Ala  
85 90 95  
Glu Glu Leu Val Gly Gln Glu Val Leu Tyr Lys Leu Thr Ser Glu Asn  
100 105 110  
Cys Glu His Phe Val Asn Glu Leu Arg Tyr Gly Val Ala Arg Ser Asp  
115 120 125  
Gln Val Arg Asp Val Ile Ile Ala Ala Ser Val Ala Gly Met Gly Leu  
130 135 140  
Ala Ala Met Ser Leu Ile Gly Val Met Phe Ser Arg Asn Lys Arg Gln  
145 150 155 160  
Lys Gln

<210> 27  
<211> 162  
<212> PRT  
<213> Homo sapiens

<400> 27

Met Arg Ala Pro Ile Pro Glu Pro Lys Pro Gly Asp Leu Ile Glu Ile  
1 5 10 15  
Phe Arg Pro Phe Tyr Arg His Trp Ala Ile Tyr Val Gly Asp Gly Tyr  
20 25 30  
Val Val His Leu Ala Pro Pro Ser Glu Val Ala Gly Ala Gly Ala Ala  
35 40 45  
Ser Val Met Ser Ala Leu Thr Asp Lys Ala Ile Val Lys Lys Glu Leu  
50 55 60  
Leu Tyr Asp Val Ala Gly Ser Asp Lys Tyr Gln Val Asn Asn Lys His  
65 70 75 80

Asp Asp Lys Tyr Ser Pro Leu Pro Cys Thr Lys Ile Ile Gln Arg Ala  
                     85                    90                    95  
 Glu Glu Leu Val Gly Gln Glu Val Leu Tyr Lys Leu Thr Ser Glu Asn  
                     100                    105                    110  
 Cys Glu His Phe Val Asn Glu Leu Arg Tyr Gly Val Ala Arg Ser Asp  
                     115                    120                    125  
 Gln Val Arg Asp Val Ile Ile Ala Ala Ser Val Ala Gly Met Gly Leu  
                     130                    135                    140  
 Ala Ala Met Ser Leu Ile Gly Val Met Phe Ser Arg Asn Lys Arg Gln  
                     145                    150                    155                    160  
 Lys Gln

<210> 28  
 <211> 64  
 <212> PRT  
 <213> Nematode

<400> 28  
 Met Ala Pro Lys Gln Arg Met Thr Leu Ala Asn Lys Gln Phe Ser Lys  
                     1                    5                    10                    15  
 Asn Val Asn Asn Arg Gly Asn Val Ala Lys Ser Leu Lys Pro Ala Glu  
                     20                    25                    30  
 Asp Lys Tyr Pro Ala Ala Pro Trp Leu Ile Gly Leu Phe Val Phe Val  
                     35                    40                    45  
 Val Cys Gly Ser Ala Val Phe Glu Ile Ile Arg Tyr Val Lys Met Gly  
                     50                    55                    60

<210> 29  
 <211> 162  
 <212> PRT  
 <213> Homo sapiens

<400> 29  
 Met Arg Ala Pro Ile Pro Glu Pro Lys Pro Gly Asp Leu Ile Glu Ile  
                     1                    5                    10                    15  
 Phe Arg Pro Phe Tyr Arg His Trp Ala Ile Tyr Val Gly Asp Gly Tyr  
                     20                    25                    30  
 Val Val His Leu Ala Pro Pro Ser Glu Val Ala Gly Ala Gly Ala Ala  
                     35                    40                    45  
 Ser Val Met Ser Ala Leu Thr Asp Lys Ala Ile Val Lys Lys Glu Leu  
                     50                    55                    60  
 Leu Tyr Asp Val Ala Gly Ser Asp Lys Tyr Gln Val Asn Asn Lys His  
                     65                    70                    75                    80  
 Asp Asp Lys Tyr Ser Pro Leu Pro Cys Thr Lys Ile Ile Gln Arg Ala  
                     85                    90                    95  
 Glu Glu Leu Val Gly Gln Glu Val Leu Tyr Lys Leu Thr Ser Glu Asn  
                     100                    105                    110

Cys Glu His Phe Val Asn Glu Leu Arg Tyr Gly Val Ala Arg Ser Asp  
 115 120 125  
 Gln Val Arg Asp Val Ile Ile Ala Ala Ser Val Ala Gly Met Gly Leu  
 130 135 140  
 Ala Ala Met Ser Leu Ile Gly Val Met Phe Ser Arg Asn Lys Arg Gln  
 145 150 155 160  
 Lys Gln

<210> 30  
 <211> 185  
 <212> PRT  
 <213> Nematode

<220>  
 <221>  
 <222> 150  
 <223> Unknown

<400> 30  
 Met Arg Ala Pro Ile Pro Glu Pro Lys Pro Gly Asp Leu Ile Glu Ile  
 1 5 10 15  
 Phe Arg Pro Phe Tyr Arg His Trp Ala Ile Tyr Val Gly Asp Gly Tyr  
 20 25 30  
 Val Val His Leu Ala Pro Pro Ser Glu Val Ala Gly Ala Gly Ala Ala  
 35 40 45  
 Ser Val Met Ser Ala Leu Thr Asp Lys Ala Ile Val Lys Lys Glu Leu  
 50 55 60  
 Leu Tyr Asp Val Ala Gly Ser Asp Lys Tyr Gln Val Asn Asn Lys His  
 65 70 75 80  
 Asp Asp Lys Tyr Ser Pro Leu Pro Cys Thr Lys Ile Ile Gln Arg Ala  
 85 90 95  
 Glu Glu Leu Val Gly Gln Glu Val Leu Tyr Lys Leu Thr Ser Glu Asn  
 100 105 110  
 Cys Glu His Phe Val Asn Glu Leu Met Ala Pro Lys Gln Arg Met Thr  
 115 120 125  
 Leu Ala Asn Lys Gln Phe Ser Lys Asn Val Asn Asn Arg Gly Asn Val  
 130 135 140  
 Ala Lys Ser Leu Lys Xaa Pro Ala Glu Asp Lys Tyr Pro Ala Ala Pro  
 145 150 155 160  
 Trp Leu Ile Gly Leu Phe Val Phe Val Val Cys Gly Ser Ala Val Phe  
 165 170 175  
 Glu Ile Ile Arg Tyr Val Lys Met Gly  
 180 185